

SEQUENCE LISTING

<110> Thibeault, Diane
 Lamarre, Daniel
 Maurice, Roger
 Pilote, Louise
 Pause, Armin

<120> Purified Active HCV NS2/3 Protease

<130> 13/082-1-D1

<150> US 10/017,736

<151> 2001-12-14

<150> US 60/256,031

<151> 2000-12-15

<160> 25

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1230

<212> DNA

<213> HCV

<220>

<221> CDS

<222> (1)...(1230)

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Met Asp Arg Glu Met Ala Ala Ser Cys Gly Gly Ala Val Phe Ile Gly	
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ctt gca ctc ttg acc ttg tca cca tac tat aaa gtg ctc ctc gct agg	96
Leu Ala Leu Leu Thr Leu Ser Pro Tyr Tyr Lys Val Leu Leu Ala Arg	
20 25 30	
ctc ata tgg tgg tta cag tat tta atc acc aga gtc gag gcg cac ttg	144
Leu Ile Trp Trp Leu Gln Tyr Leu Ile Thr Arg Val Glu Ala His Leu	
35 40 45	
caa gtg tgg atc ccc cct ctc aat gtt cgg gga ggc cgc gat gcc atc	192
Gln Val Trp Ile Pro Pro Leu Asn Val Arg Gly Gly Arg Asp Ala Ile	
50 55 60	
atc ctc ctc acg tgc gca gtc cac cca gag cta atc ttt gac atc acc	240
Ile Leu Leu Thr Cys Ala Val His Pro Glu Leu Ile Phe Asp Ile Thr	
65 70 75 80	
aaa ctc ctg ctc gcc ata ttc ggt ccg ctc atg gtg ctc cag gca ggc	288
Lys Leu Leu Leu Ala Ile Phe Gly Pro Leu Met Val Leu Gln Ala Gly	
85 90 95	
ata acc aaa gtg ccg tac ttc gtg cgt gcg cag ggg ctc att cgt gcg	336
Ile Thr Lys Val Pro Tyr Phe Val Arg Ala Gln Gly Leu Ile Arg Ala	

100										105										110										
tgt atg ttg gtg cgg aag gct gcg ggg ggt cat tat gtc caa atg gcc	384																													
Cys Met Leu Val Arg Lys Ala Ala Gly Gly His Tyr Val Gln Met Ala																														
115 120 125																														
ttc atg aag cta gct gcg ctg aca ggt acg tac gtt tat gac cat ctc	432																													
Phe Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp His Leu																														
130 135 140																														
act cca ttg cag gat tgg gcc cac gcg ggc cta cga gac ctt gca gtg	480																													
Thr Pro Leu Gln Asp Trp Ala His Ala Gly Leu Arg Asp Leu Ala Val																														
145 150 155 160																														
gcg gta gag ccc gtc atc ttc tct gac atg gag gtc aag atc atc acc	528																													
Ala Val Glu Pro Val Ile Phe Ser Asp Met Glu Val Lys Ile Ile Thr																														
165 170 175																														
tgg ggg gcg gac acc gcg gca tgc ggg gac atc att tca ggt ctg ccc	576																													
Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Ser Gly Leu Pro																														
180 185 190																														
gtc tcc gct cga agg gga agg gag ata ctc ctg gga ccg gcc gat aat	624																													
Val Ser Ala Arg Arg Gly Arg Glu Ile Leu Leu Gly Pro Ala Asp Asn																														
195 200 205																														
ttt gaa ggg cag ggg tgg cga ctc ctt gcg ccc atc acg gcc tac tcc	672																													
Phe Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala Tyr Ser																														
210 215 220																														
caa cag aca cgg ggc cta ctt ggt tgc atc atc acc agc ctc aca ggc	720																													
Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly																														
225 230 235 240																														
cgg gac aag aac cag gtc gag ggg gag gtt caa gtg gtc tcc acc gct	768																													
Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala																														
245 250 255																														
aca caa tct ttc ctg gcg acc tgc gtc aac ggc gtg tgt tgg act gtc	816																													
Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val																														
260 265 270																														
ttc cat ggc gcc ggc tca aag acc ttg gcc ggc ccc aaa ggc cca atc	864																													
Phe His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile																														
275 280 285																														
acc cag atg tac act aat gtg gac cag gac ctc gtc ggc tgg cag gcg	912																													
Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala																														
290 295 300																														
ccc cct ggg gcg cgc tcc atg aca cca tgc acc tgc ggc agc tcg gac	960																													
Pro Pro Gly Ala Arg Ser Met Thr Pro Cys Thr Cys Gly Ser Ser Asp																														
305 310 315 320																														
ctc tat ttg gtc acg aga cat gcc gac gtc att ccg gtg cgc cgg cgg	1008																													
Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg																														
325 330 335																														

ggc gac agt agg ggg agc ctg ctc tcc ccc agg cct gtc tcc tac ttg	1056 Gly
Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu	
340 345 350	
aag ggc tct tcg ggt ggc cca ctg ctc tgc cct tcg ggg cac gct gtg	1104
Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val	
355 360 365	
ggc atc ttc cgg gct gct gtg tgc acc cgg ggg gtt gca aaa gcg gtg	1152
Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val	
370 375 380	
gac ttc ata cct gtt gag tct atg gaa act acc atg cgg act agt agc	1200
Asp Phe Ile Pro Val Glu Ser Met Glu Thr Thr Met Arg Thr Ser Ser	
385 390 395 400	
gct tgg cgt cac ccg cag ttc ggt ggt taa	1230
Ala Trp Arg His Pro Gln Phe Gly Gly *	
405	

<210> 2
 <211> 409
 <212> PRT
 <213> HCV

<400> 2

Met Asp Arg Glu Met Ala Ala Ser Cys Gly Gly Ala Val Phe Ile Gly	
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Leu Ala Leu Leu Thr Leu Ser Pro Tyr Tyr Lys Val Leu Leu Ala Arg	
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Leu Ile Trp Trp Leu Gln Tyr Leu Ile Thr Arg Val Glu Ala His Leu	
35 40 45	
Gln Val Trp Ile Pro Pro Leu Asn Val Arg Gly Gly Arg Asp Ala Ile	
50 55 60	
Ile Leu Leu Thr Cys Ala Val His Pro Glu Leu Ile Phe Asp Ile Thr	
65 70 75 80	
Lys Leu Leu Leu Ala Ile Phe Gly Pro Leu Met Val Leu Gln Ala Gly	
85 90 95	
Ile Thr Lys Val Pro Tyr Phe Val Arg Ala Gln Gly Leu Ile Arg Ala	
100 105 110	
Cys Met Leu Val Arg Lys Ala Ala Gly Gly His Tyr Val Gln Met Ala	
115 120 125	
Phe Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp His Leu	
130 135 140	
Thr Pro Leu Gln Asp Trp Ala His Ala Gly Leu Arg Asp Leu Ala Val	
145 150 155 160	
Ala Val Glu Pro Val Ile Phe Ser Asp Met Glu Val Lys Ile Ile Thr	
165 170 175	

Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Ser Gly Leu Pro
 180 185 190
 Val Ser Ala Arg Arg Gly Arg Glu Ile Leu Leu Gly Pro Ala Asp Asn
 195 200 205
 Phe Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala Tyr Ser
 210 215 220
 Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly
 225 230 235 240
 Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala
 245 250 255
 Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val
 260 265 270
 Phe His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile
 275 280 285
 Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala
 290 295 300
 Pro Pro Gly Ala Arg Ser Met Thr Pro Cys Thr Cys Gly Ser Ser Asp
 305 310 315 320
 Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg
 325 330 335
 Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu
 340 345 350
 Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val
 355 360 365
 Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val
 370 375 380
 Asp Phe Ile Pro Val Glu Ser Met Glu Thr Thr Met Arg Thr Ser Ser
 385 390 395 400
 Ala Trp Arg His Pro Gln Phe Gly Gly
 405

<210> 3
 <211> 1011
 <212> DNA
 <213> HCV

<220>
 <221> CDS
 <222> (1)...(1005)

<400> 3
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 Met Lys Lys Lys Lys Leu Glu His His His His His His Thr Ser Ala
 1 5 10 15

ggc ata acc aaa gtg ccg tac ttc gtg cgt gcg cag ggg ctc att cgt	96
Gly Ile Thr Lys Val Pro Tyr Phe Val Arg Ala Gln Gly Leu Ile Arg	
20 25 30	
gcg tgt atg ttg gtg cgg aag gct gcg ggg ggt cat tat gtc caa atg	144
Ala Cys Met Leu Val Arg Lys Ala Ala Gly Gly His Tyr Val Gln Met	
35 40 45	
gcc ttc atg aag cta gct gcg ctg aca ggt acg tac gtt tat gac cat	192
Ala Phe Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp His	
50 55 60	
ctc act cca ttg cag gat tgg gcc cac gcg ggc cta cga gac ctt gca	240
Leu Thr Pro Leu Gln Asp Trp Ala His Ala Gly Leu Arg Asp Leu Ala	
65 70 75 80	
gtg gcg gta gag ccc gtc atc ttc tct gac atg gag gtc aag atc atc	288
Val Ala Val Glu Pro Val Ile Phe Ser Asp Met Glu Val Lys Ile Ile	
85 90 95	
acc tgg ggg gcg gac acc gcg gca tgc ggg gac atc att tca ggt ctg	336
Thr Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Ser Gly Leu	
100 105 110	
ccc gtc tcc gct cga agg gga agg gag ata ctc ctg gga ccg gcc gat	384
Pro Val Ser Ala Arg Arg Gly Arg Glu Ile Leu Leu Gly Pro Ala Asp	
115 120 125	
aat ttt gaa ggg cag ggg tgg cga ctc ctt gcg ccc atc acg gcc tac	432
Asn Phe Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala Tyr	
130 135 140	
tcc caa cag aca cgg gcc cta ctt ggt tgc atc atc acc agc ctc aca	480
Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr	
145 150 155 160	
ggc cgg gac aag aac cag gtc gag ggg gag gtt caa gtg gtc tcc acc	528
Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr	
165 170 175	
gct aca caa tct ttc ctg gcg acc tgc gtc aac ggc gtg tgt tgg act	576
Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr	
180 185 190	
gtc ttc cat ggc gcc ggc tca aag acc ttg gcc ggc ccc aaa ggc cca	624
Val Phe His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro	
195 200 205	
atc acc cag atg tac act aat gtg gac cag gac ctc gtc ggc tgg cag	672
Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln	
210 215 220	
gcg ccc cct ggg gcg cgc tcc atg aca cca tgc acc tgc ggc agc tcg	720
Ala Pro Pro Gly Ala Arg Ser Met Thr Pro Cys Thr Cys Gly Ser Ser	
225 230 235 240	
gac ctc tat ttg gtc acg aga cat gcc gac gtc att ccg gtg cgc cgg	768
Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg	
245 250 255	

cgg ggc gac agt agg ggg agc ctg ctc tcc ccc agg cct gtc tcc tac Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr 260 265 270	816
ttg aag ggc tct tcg ggt ggc cca ctg ctc tgc cct tcg ggg cac gct Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala 275 280 285	864
gtg ggc atc ttc cgg gct gct gtg tgc acc cgg ggg gtt gca aaa gcg Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala 290 295 300	912
gtg gac ttc ata cct gtt gag tct atg gaa act acc atg cgg act agt Val Asp Phe Ile Pro Val Glu Ser Met Glu Thr Thr Met Arg Thr Ser 305 310 315 320	960
agc gct tgg cgt cac ccg cag ttc ggt ggt aaa aag aaa aag taa Ser Ala Trp Arg His Pro Gln Phe Gly Gly Lys Lys Lys Lys * 325 330	1005
ggatcc	1011

<210> 4
<211> 334
<212> PRT
<213> HCV

<400> 4
Met Lys Lys Lys Lys Leu Glu His His His His His His Thr Ser Ala
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20 25 30
Ala Cys Met Leu Val Arg Lys Ala Ala Gly Gly His Tyr Val Gln Met
35 40 45
Ala Phe Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp His
50 55 60
Leu Thr Pro Leu Gln Asp Trp Ala His Ala Gly Leu Arg Asp Leu Ala
65 70 75 80
Val Ala Val Glu Pro Val Ile Phe Ser Asp Met Glu Val Lys Ile Ile
85 90 95
Thr Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Ser Gly Leu
100 105 110
Pro Val Ser Ala Arg Arg Gly Arg Glu Ile Leu Leu Gly Pro Ala Asp
115 120 125
Asn Phe Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala Tyr
130 135 140
Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr
145 150 155 160
Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr

165										170					175				
Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr				
			180					185					190						
Val	Phe	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro				
		195					200					205							
Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln				
	210					215					220								
Ala	Pro	Pro	Gly	Ala	Arg	Ser	Met	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser				
225					230					235					240				
Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg				
				245					250					255					
Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr				
			260					265					270						
Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala				
		275					280					285							
Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala				
	290					295					300								
Val	Asp	Phe	Ile	Pro	Val	Glu	Ser	Met	Glu	Thr	Thr	Met	Arg	Thr	Ser				
305					310					315					320				
Ser	Ala	Trp	Arg	His	Pro	Gln	Phe	Gly	Gly	Lys	Lys	Lys	Lys						
				325					330										

<210> 5
 <211> 20
 <212> DNA
 <213> HCV

<400> 5
 ccatggaccg ggagatggct

20

<210> 6
 <211> 63
 <212> DNA
 <213> HCV

<400> 6
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 cat 63

<210> 7
 <211> 46
 <212> DNA
 <213> HCV

<400> 7
 gctcgagcat caccatcacc atcacactag tgcaggcata accaaa

46

<210> 8
 <211> 45
 <212> DNA
 <213> HCV

<400> 8
 aacaatggat ccttactttt tctttttacc accgaactgc ggggtg 45

<210> 9
 <211> 45
 <212> DNA
 <213> HCV

<400> 9
 acctgccata tgaaaaagaa aaagctcgag catcaccatc accat 45

<210> 10
 <211> 303
 <212> PRT
 <213> HCV

<400> 10
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 20 25 30
 Met Ala Phe Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp
 35 40 45
 His Leu Thr Pro Leu Gln Asp Trp Ala His Ala Gly Leu Arg Asp Leu
 50 55 60
 Ala Val Ala Val Glu Pro Val Ile Phe Ser Asp Met Glu Val Lys Ile
 65 70 75 80
 Ile Thr Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Ser Gly
 85 90 95
 Leu Pro Val Ser Ala Arg Arg Gly Arg Glu Ile Leu Leu Gly Pro Ala
 100 105 110
 Asp Asn Phe Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala
 115 120 125
 Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu
 130 135 140
 Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser
 145 150 155 160
 Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp
 165 170 175
 Thr Val Phe His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly
 180 185 190

Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp
 195 200 205
 Gln Ala Pro Pro Gly Ala Arg Ser Met Thr Pro Cys Thr Cys Gly Ser
 210 215 220
 Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg
 225 230 235 240
 Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser
 245 250 255
 Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His
 260 265 270
 Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys
 275 280 285
 Ala Val Asp Phe Ile Pro Val Glu Ser Met Glu Thr Thr Met Arg
 290 295 300

<210> 11
 <211> 393
 <212> PRT
 <213> HCV

<400> 11
 Met Ala Ala Ser Cys Gly Gly Ala Val Phe Ile Gly Leu Ala Leu Leu
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 Thr Leu Ser Pro Tyr Tyr Lys Val Leu Leu Ala Arg Leu Ile Trp Trp
 20 25 30
 Leu Gln Tyr Leu Ile Thr Arg Val Glu Ala His Leu Gln Val Trp Ile
 35 40 45
 Pro Pro Leu Asn Val Arg Gly Gly Arg Asp Ala Ile Ile Leu Leu Thr
 50 55 60
 Cys Ala Val His Pro Glu Leu Ile Phe Asp Ile Thr Lys Leu Leu Leu
 65 70 75 80
 Ala Ile Phe Gly Pro Leu Met Val Leu Gln Ala Gly Ile Thr Lys Val
 85 90 95
 Pro Tyr Phe Val Arg Ala Gln Gly Leu Ile Arg Ala Cys Met Leu Val
 100 105 110
 Arg Lys Ala Ala Gly Gly His Tyr Val Gln Met Ala Phe Met Lys Leu
 115 120 125
 Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp His Leu Thr Pro Leu Gln
 130 135 140
 Asp Trp Ala His Ala Gly Leu Arg Asp Leu Ala Val Ala Val Glu Pro
 145 150 155 160
 Val Ile Phe Ser Asp Met Glu Val Lys Ile Ile Thr Trp Gly Ala Asp

Leu Leu Thr Cys Ala Val His Pro Glu Leu Ile Phe Asp Ile Thr Lys
 50 55 60
 Leu Leu Leu Ala Ile Phe Gly Pro Leu Met Val Leu Gln Ala Gly Ile
 65 70 75 80
 Thr Lys Val Pro Tyr Phe Val Arg Ala Gln Gly Leu Ile Arg Ala Cys
 85 90 95
 Met Leu Val Arg Lys Ala Ala Gly Gly His Tyr Val Gln Met Ala Phe
 100 105 110
 Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp His Leu Thr
 115 120 125
 Pro Leu Gln Asp Trp Ala His Ala Gly Leu Arg Asp Leu Ala Val Ala
 130 135 140
 Val Glu Pro Val Ile Phe Ser Asp Met Glu Val Lys Ile Ile Thr Trp
 145 150 155 160
 Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Ser Gly Leu Pro Val
 165 170 175
 Ser Ala Arg Arg Gly Arg Glu Ile Leu Leu Gly Pro Ala Asp Asn Phe
 180 185 190
 Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala Tyr Ser Gln
 195 200 205
 Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg
 210 215 220
 Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr
 225 230 235 240
 Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val Phe
 245 250 255
 His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr
 260 265 270
 Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro
 275 280 285
 Pro Gly Ala Arg Ser Met Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu
 290 295 300
 Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg Gly
 305 310 315 320
 Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys
 325 330 335
 Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly
 340 345 350
 Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp
 355 360 365

Phe Ile Pro Val Glu Ser Met Glu Thr Thr Met Arg
 370 375 380

<210> 13
 <211> 352
 <212> PRT
 <213> HCV

<400> 13
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 Asp Ala Ile Ile Leu Leu Thr Cys Ala Val His Pro Glu Leu Ile Phe
 20 25 30
 Asp Ile Thr Lys Leu Leu Leu Ala Ile Phe Gly Pro Leu Met Val Leu
 35 40 45
 Gln Ala Gly Ile Thr Lys Val Pro Tyr Phe Val Arg Ala Gln Gly Leu
 50 55 60
 Ile Arg Ala Cys Met Leu Val Arg Lys Ala Ala Gly Gly His Tyr Val
 65 70 75 80
 Gln Met Ala Phe Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr
 85 90 95
 Asp His Leu Thr Pro Leu Gln Asp Trp Ala His Ala Gly Leu Arg Asp
 100 105 110
 Leu Ala Val Ala Val Glu Pro Val Ile Phe Ser Asp Met Glu Val Lys
 115 120 125
 Ile Ile Thr Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Ser
 130 135 140
 Gly Leu Pro Val Ser Ala Arg Arg Gly Arg Glu Ile Leu Leu Gly Pro
 145 150 155 160
 Ala Asp Asn Phe Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr
 165 170 175
 Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser
 180 185 190
 Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val
 195 200 205
 Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys
 210 215 220
 Trp Thr Val Phe His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys
 225 230 235 240
 Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly
 245 250 255
 Trp Gln Ala Pro Pro Gly Ala Arg Ser Met Thr Pro Cys Thr Cys Gly
 260 265 270

Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val
 275 280 285
 Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val
 290 295 300
 Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly
 305 310 315 320
 His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala
 325 330 335
 Lys Ala Val Asp Phe Ile Pro Val Glu Ser Met Glu Thr Thr Met Arg
 340 345 350

 <210> 14
 <211> 341
 <212> PRT
 <213> HCV

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 Val Arg Gly Gly Arg Asp Ala Ile Ile Leu Leu Thr Cys Ala Val His
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 Pro Glu Leu Ile Phe Asp Ile Thr Lys Leu Leu Leu Ala Ile Phe Gly
 20 25 30
 Pro Leu Met Val Leu Gln Ala Gly Ile Thr Lys Val Pro Tyr Phe Val
 35 40 45
 Arg Ala Gln Gly Leu Ile Arg Ala Cys Met Leu Val Arg Lys Ala Ala
 50 55 60
 Gly Gly His Tyr Val Gln Met Ala Phe Met Lys Leu Ala Ala Leu Thr
 65 70 75 80
 Gly Thr Tyr Val Tyr Asp His Leu Thr Pro Leu Gln Asp Trp Ala His
 85 90 95
 Ala Gly Leu Arg Asp Leu Ala Val Ala Val Glu Pro Val Ile Phe Ser
 100 105 110
 Asp Met Glu Val Lys Ile Ile Thr Trp Gly Ala Asp Thr Ala Ala Cys
 115 120 125
 Gly Asp Ile Ile Ser Gly Leu Pro Val Ser Ala Arg Arg Gly Arg Glu
 130 135 140
 Ile Leu Leu Gly Pro Ala Asp Asn Phe Glu Gly Gln Gly Trp Arg Leu
 145 150 155 160
 Leu Ala Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly
 165 170 175
 Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly
 180 185 190
 Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys

195					200					205					
Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Phe	His	Gly	Ala	Gly	Ser	Lys	Thr
210					215					220					
Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp
225				230				235				240			
Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Met	Thr
				245				250				255			
Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala
				260				265				270			
Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu
				275				280				285			
Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu
				290				295				300			
Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys
305				310				315				320			
Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Ile	Pro	Val	Glu	Ser	Met
				325				330				335			
Glu	Thr	Thr	Met	Arg											
340															

<210> 15
 <211> 292
 <212> PRT
 <213> HCV

<400> 15

Ala	Gln	Gly	Leu	Ile	Arg	Ala	Cys	Met	Leu	Val	Arg	Lys	Ala	Ala	Gly
1				5					10					15	
Gly	His	Tyr	Val	Gln	Met	Ala	Phe	Met	Lys	Leu	Ala	Ala	Leu	Thr	Gly
			20				25				30				
Thr	Tyr	Val	Tyr	Asp	His	Leu	Thr	Pro	Leu	Gln	Asp	Trp	Ala	His	Ala
			35				40				45				
Gly	Leu	Arg	Asp	Leu	Ala	Val	Ala	Val	Glu	Pro	Val	Ile	Phe	Ser	Asp
50			55			60									
Met	Glu	Val	Lys	Ile	Ile	Thr	Trp	Gly	Ala	Asp	Thr	Ala	Ala	Cys	Gly
65				70				75				80			
Asp	Ile	Ile	Ser	Gly	Leu	Pro	Val	Ser	Ala	Arg	Arg	Gly	Arg	Glu	Ile
				85				90				95			
Leu	Leu	Gly	Pro	Ala	Asp	Asn	Phe	Glu	Gly	Gln	Gly	Trp	Arg	Leu	Leu
100				105				110							
Ala	Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys
115				120				125							

Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu
 130 135 140
 Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val
 145 150 155 160
 Asn Gly Val Cys Trp Thr Val Phe His Gly Ala Gly Ser Lys Thr Leu
 165 170 175
 Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln
 180 185 190
 Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Met Thr Pro
 195 200 205
 Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp
 210 215 220
 Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser
 225 230 235 240
 Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu
 245 250 255
 Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr
 260 265 270
 Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Ser Met Glu
 275 280 285
 Thr Thr Met Arg
 290

<210> 16
 <211> 303
 <212> PRT
 <213> HCV

<400> 16
 Ala Gly Ile Thr Lys Val Pro Tyr Phe Val Arg Ala Gln Gly Leu Ile
 1 5 10 15
 Arg Ala Cys Met Leu Val Arg Lys Ala Ala Gly Gly His Tyr Val Gln
 20 25 30
 Met Ala Phe Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp
 35 40 45
 Ala Leu Thr Pro Leu Gln Asp Trp Ala His Ala Gly Leu Arg Asp Leu
 50 55 60
 Ala Val Ala Val Glu Pro Val Ile Phe Ser Asp Met Glu Val Lys Ile
 65 70 75 80
 Ile Thr Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Ser Gly
 85 90 95
 Leu Pro Val Ser Ala Arg Arg Gly Arg Glu Ile Leu Leu Gly Pro Ala
 100 105 110

Asp Asn Phe Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala
 115 120 125
 Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu
 130 135 140
 Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser
 145 150 155 160
 Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp
 165 170 175
 Thr Val Phe His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly
 180 185 190
 Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp
 195 200 205
 Gln Ala Pro Pro Gly Ala Arg Ser Met Thr Pro Cys Thr Cys Gly Ser
 210 215 220
 Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg
 225 230 235 240
 Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser
 245 250 255
 Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His
 260 265 270
 Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys
 275 280 285
 Ala Val Asp Phe Ile Pro Val Glu Ser Met Glu Thr Thr Met Arg
 290 295 300

<210> 17
 <211> 301
 <212> PRT
 <213> HCV

<400> 17
 Ala Gly Ile Thr Lys Val Pro Tyr Phe Val Arg Ala Gln Gly Leu Ile
 1 5 10 15
 Arg Ala Cys Met Leu Val Arg Lys Ala Ala Gly Gly His Tyr Val Gln
 20 25 30
 Met Ala Phe Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp
 35 40 45
 His Leu Thr Pro Leu Gln Asp Trp Ala His Ala Gly Leu Arg Asp Leu
 50 55 60
 Ala Val Ala Val Glu Pro Val Ile Phe Ser Asp Met Glu Val Lys Ile
 65 70 75 80
 Ile Thr Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Ser Gly

85										90					95				
Leu	Pro	Val	Ser	Ala	Arg	Arg	Gly	Arg	Glu	Ile	Leu	Leu	Gly	Pro	Ala				
			100					105					110						
Asp	Asn	Phe	Glu	Gly	Gln	Gly	Trp	Arg	Leu	Pro	Ile	Thr	Ala	Tyr	Ser				
		115					120					125							
Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly				
	130					135					140								
Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala				
145					150					155					160				
Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val				
				165					170					175					
Phe	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile				
			180					185					190						
Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala				
		195					200					205							
Pro	Pro	Gly	Ala	Arg	Ser	Met	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp				
	210					215					220								
Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg				
225					230				235						240				
Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu				
				245					250					255					
Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val				
			260				265						270						
Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val				
	275					280						285							
Asp	Phe	Ile	Pro	Val	Glu	Ser	Met	Glu	Thr	Thr	Met	Arg							
	290					295					300								

<210> 18
 <211> 303
 <212> PRT
 <213> HCV

<400> 18
 Ala Gly Ile Thr Lys Val Pro Tyr Phe Val Arg Ala Gln Gly Leu Ile
 1 5 10 15
 Arg Ala Cys Met Leu Val Arg Lys Ala Ala Gly Gly His Tyr Val Gln
 20 25 30
 Met Ala Phe Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp
 35 40 45
 His Leu Thr Pro Leu Gln Asp Trp Ala His Ala Gly Leu Arg Asp Leu
 50 55 60

Ala Val Ala Val Glu Pro Val Ile Phe Ser Asp Met Glu Val Lys Ile
 65 70 75 80
 Ile Thr Trp Gly Ala Asp Thr Ala Ala Ala Gly Asp Ile Ile Ser Gly
 85 90 95
 Leu Pro Val Ser Ala Arg Arg Gly Arg Glu Ile Leu Leu Gly Pro Ala
 100 105 110
 Asp Asn Phe Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala
 115 120 125
 Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu
 130 135 140
 Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser
 145 150 155 160
 Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp
 165 170 175
 Thr Val Phe His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly
 180 185 190
 Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp
 195 200 205
 Gln Ala Pro Pro Gly Ala Arg Ser Met Thr Pro Cys Thr Cys Gly Ser
 210 215 220
 Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg
 225 230 235 240
 Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser
 245 250 255
 Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His
 260 265 270
 Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys
 275 280 285
 Ala Val Asp Phe Ile Pro Val Glu Ser Met Glu Thr Thr Met Arg
 290 295 300

<210> 19

<211> 11

<212> PRT

<213> HCV

<220>

<221> VARIANT

<222> (1)...(1)

<223> Asp labeled with anthranilyl

<221> VARIANT

<222> (6)...(6)

<223> Xaa at position 6 is Abu

<221> VARIANT
 <222> (6)...(7)
 <223> Abu-A between 6 and 7 is C(O)-O
 <221> VARIANT
 <222> (9)...(9)
 <223> Tyr at position 9 is derivatized with 3-NO2

<400> 19
 Asp Asp Ile Val Pro Xaa Ala Met Tyr Thr Trp
 1 5 10

<210> 20
 <211> 6
 <212> PRT
 <213> HCV

<220>
 <221> VARIANT
 <222> (1)...(1)
 <223> Asp labeled with anthranilyl

<221> VARIANT
 <222> (6)...(6)
 <223> Xaa at position 6 is Abu

<400> 20
 Asp Asp Ile Val Pro Xaa
 1 5

<210> 21
 <211> 10
 <212> PRT
 <213> HCV

<400> 21
 Ser Phe Glu Gly Gln Gly Trp Arg Leu Leu
 1 5 10

<210> 22
 <211> 20
 <212> PRT
 <213> HCV

<400> 22
 Ser Phe Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala Tyr
 1 5 10 15

Ser Gln Gln Thr
 20

<210> 23
 <211> 10
 <212> PRT
 <213> HCV

<400> 23

Ala Pro Ile Thr Ala Tyr Ser Gln Gln Thr
1 5 10

<210> 24
<211> 12
<212> PRT
<213> HCV

<400> 24
Lys Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala Tyr
1 5 10

<210> 25
<211> 6
<212> PRT
<213> HCV

<400> 25
Ala Pro Ile Thr Ala Tyr
1 5